Tavazza.ST25.txt
SEQUENCE LISTING

<110> ENEA-Ente per le Nuove Tecnologie e l'Ambiente
       Consiglio Nazionale delle Ricerche

<120> Method for the preparation of transgenic plants characterised by
       Geminivirus lasting resistance

<130> PCT25622

<140> RM2003A000242
<141> 2003-05-19

<150> RM2003A000242
<151> 2003-05-19

<160> 12

<170> PatentIn version 3.2

<210> 1
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<212> DNA
<213> Geminivirus TYLCSV

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aaattattca tcaaaatttg cagagaacta catgaaaatg gggaacctca tctccatatt   180

ctcatccaat tcgaaggaaa atacaattgt accaatcaac gattcttcga cctggtatcc   240

ccaaccaggt cagcacattt ccatccgaac attcagggag ctaaatcgag ctccgacgtc   300

aagtcctata tcgacaagga cggagatgtt cttgaatggg gtactttcca gatcgacgga   360

cgatctgcta ggggaggaca acagacagcc aacgacgctt acgcaaaggc aattaacgca   420

ggaagtaagt cgcaggctct tgatgtaatt aaagaattag cgcctagaga ttacgttcta   480

cattttcata atataaatag taatttagat aaggttttcc aggtgcctcc ggcaccttat   540

gtttctcctt ttttatcttc ttctttcgat caagttcctg atgaacttga acactgggtt   600

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1   5   10   15

aca tac ccc aag tgt gac tta act aag gag aat gca ttg tcc cag ata   96
                                 Pagina 1

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                                          Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
                                                   20              25                  30

act aac ttg caa act ccc act aac aag ttg ttc att aag att tgt agg    144
Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
             35              40                  45

gaa ctt cat gag aat gga gaa cca cat ctt cat atc ttg ata cag ttc    192
Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
         50              55                  60

gaa ggc aag tat aac tgc acc aac caa cgt ttc ttt gac ctt gtg tcc    240
Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
65               70                  75                  80

cct acc aga tca gcc cat ttt cat cca aac atc cag ggt gct aag tcg    288
Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                 85                  90                  95

agt tca gac gtg aag tca tac att gac aaa gac ggc gat gtg ctc gag    336
Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
                 100                 105                 110

tgg gga act ttt cag ata gac ggt cga tcg gct aga gga ggt cag caa    384
Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
             115                 120                 125

aca gct aac gat gca tac gct aag gct atc aac gct gga tcc aag tca    432
Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser
         130                 135                 140

cag gca ctt gac gta atc aaa gag tta gct cct agg gat tat gtt ctt    480
Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu
145                 150                 155                 160

cat ttc cat aac atc aac agc aat ttg gac aaa gtg ttc caa gtg cca    528
His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro
                 165                 170                 175

ccg gct cct tac gtt tca cct ttc tta agt tct tca ttt gat cag gtt    576
Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val
             180                 185                 190

cca gat gag ctt gag cat tgg gtg tcc gaa aac gtt atg gac gcc gca    624
Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala Ala
             195                 200                 205

gcg cgt                                                            630
Ala Arg
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Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
             20              25                  30
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Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
            35   40   45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
        50   55   60

Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
65   70   75   80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                85   90   95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
            100   105   110

Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
        115   120   125

Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser
    130   135   140

Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu
145   150   155   160

His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro
                165   170   175

Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val
                180   185   190

Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala Ala
            195   200   205

Ala Arg
    210

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Met Pro Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu
1   5   10   15

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aca tac ccc aag tgt gac tta act aag gag aat gca ttg tcc cag ata      96
Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
             20              25                  30

act aac ttg caa act ccc act aac aag ttg ttc att aag att tgt agg     144
Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
         35              40                  45

gaa ctt cac gag aat gga gaa cca cat ctt cat atc ttg ata cag ttc     192
Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
     50              55                  60

gaa ggc aag tat aac tgc acc aac caa cgt ttc ttt gac ctt gtg tcc     240
Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
65              70              75                  80

cct acc aga tca gcc cat ttt cat cca aac atc cag ggt gct aag tcg     288
Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
                 85              90                  95

agt tca gac gtg aag tca tac att gac aaa gac ggg gat gtg ctc gag     336
Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
             100             105                 110

tgg gga act ttt cag ata gac ggt cga tcg gct aga gga ggt cag caa     384
Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
             115             120                 125

aca gca aac gat gca tac gct aag gct atc aac gct gga tcc aag tca     432
Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser
             130             135                 140

cag gca ctt gac gta atc aaa gag tta gct cct agg gat tat gtt ctt     480
Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu
145             150                 155                 160

cat ttc cat aac atc aac agc aat ttg gac aaa gtg ttc caa gtg cca     528
His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro
                 165             170                 175

ccg gct cct tac gtt tca cct ttc tta agt tct tca ttt gat cag gtt     576
Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val
             180             185                 190

cca gat gag ctt gag cat tgg gtg tct gaa aac gtt atg gac gcc gca     624
Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala Ala
         195             200             205

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gcc cgt
Ala Arg
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<223>   Synthetic Construct

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Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
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Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
        35   40   45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
    50   55   60

Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
65   70   75   80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
              85   90   95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
            100   105   110

Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
        115   120   125

Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser
    130   135   140

Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu
145   150   155   160

His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro
              165   170   175

Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val
            180   185   190

Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala Ala
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Ala Arg
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1   5   10   15

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gtg cgt agg aga ctt aac ttt gac tct ccg tac acc tct cgt gca gct        96
Val Arg Arg Arg Leu Asn Phe Asp Ser Pro Tyr Thr Ser Arg Ala Ala
            20                  25                  30

gct ccc aca gtc cag ggc att aag agg cga tct tgg aca tac aga cct       144
Ala Pro Thr Val Gln Gly Ile Lys Arg Arg Ser Trp Thr Tyr Arg Pro
            35                  40                  45

atg tac agg aaa ccg agg atg tat agg atg tat cgt agc cca gat gtg       192
Met Tyr Arg Lys Pro Arg Met Tyr Arg Met Tyr Arg Ser Pro Asp Val
        50                  55                  60

cct cct ggt tgc gaa gga ccc tgc aag gtg caa tcg tat gag caa cgt       240
Pro Pro Gly Cys Glu Gly Pro Cys Lys Val Gln Ser Tyr Glu Gln Arg
65                  70                  75                  80

gac gat gtg aag cac acc gga gtt gtt cgt tgc gtt tct gat gtg act       288
Asp Asp Val Lys His Thr Gly Val Val Arg Cys Val Ser Asp Val Thr
                85                  90                  95

aga ggt tca ggt atc act cac agg gtg gga aag cgt ttc tgt att aag       336
Arg Gly Ser Gly Ile Thr His Arg Val Gly Lys Arg Phe Cys Ile Lys
            100                 105                 110

tct att tac ata ttg ggt aag atc tgg atg gac gag aat atc aag aaa       384
Ser Ile Tyr Ile Leu Gly Lys Ile Trp Met Asp Glu Asn Ile Lys Lys
            115                 120                 125

cag aat cac act aat cag gtt atg ttc ttt ctt gtg cga gat cga aga       432
Gln Asn His Thr Asn Gln Val Met Phe Phe Leu Val Arg Asp Arg Arg
        130                 135                 140

cca tac gga acc agc cca atg gac ttc ggc cag gtg ttt aat atg ttc       480
Pro Tyr Gly Thr Ser Pro Met Asp Phe Gly Gln Val Phe Asn Met Phe
145                 150                 155                 160

gat aac gag cca tct act gca act gtg aaa aat gat ttg cgt gat aga       528
Asp Asn Glu Pro Ser Thr Ala Thr Val Lys Asn Asp Leu Arg Asp Arg
                165                 170                 175

tat cag gtg atg aga aag ttc cat gca acg gtg gtt ggt ggt cct tct       576
Tyr Gln Val Met Arg Lys Phe His Ala Thr Val Val Gly Gly Pro Ser
                180                 185                 190

gga atg aaa gag caa tgt ctt ctg aaa aga ttc ttt aag atc aac act       624
Gly Met Lys Glu Gln Cys Leu Leu Lys Arg Phe Phe Lys Ile Asn Thr
            195                 200                 205

cat gtc gtc tat aac cac cag gag caa gcg aaa tat gag aat cac act       672
His Val Val Tyr Asn His Gln Glu Gln Ala Lys Tyr Glu Asn His Thr
            210                 215                 220

gaa aat gct ttg ttg tta tac atg gcc tgt acc cac gca tct aat cca       720
Glu Asn Ala Leu Leu Leu Tyr Met Ala Cys Thr His Ala Ser Asn Pro
225                 230                 235                 240

gtt tac gca acg ctt aag atc cgt atc tat ttc tat gac gct gtg aca       768
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Asn
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<211> 257

<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

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                20   25   30

Ala Pro Thr Val Gln Gly Ile Lys Arg Arg Ser Trp Thr Tyr Arg Pro
        35   40   45

Met Tyr Arg Lys Pro Arg Met Tyr Arg Met Tyr Arg Ser Pro Asp Val
    50   55   60

Pro Pro Gly Cys Glu Gly Pro Cys Lys Val Gln Ser Tyr Glu Gln Arg
65   70   75   80

Asp Asp Val Lys His Thr Gly Val Val Arg Cys Val Ser Asp Val Thr
                85   90   95

Arg Gly Ser Gly Ile Thr His Arg Val Gly Lys Arg Phe Cys Ile Lys
                100   105   110

Ser Ile Tyr Ile Leu Gly Lys Ile Trp Met Asp Glu Asn Ile Lys Lys
            115   120   125

Gln Asn His Thr Asn Gln Val Met Phe Phe Leu Val Arg Asp Arg Arg
        130   135   140

Pro Tyr Gly Thr Ser Pro Met Asp Phe Gly Gln Val Phe Asn Met Phe
145   150   155   160

Asp Asn Glu Pro Ser Thr Ala Thr Val Lys Asn Asp Leu Arg Asp Arg
                165   170   175

Tyr Gln Val Met Arg Lys Phe His Ala Thr Val Val Gly Gly Pro Ser
            180   185   190

Gly Met Lys Glu Gln Cys Leu Leu Lys Arg Phe Phe Lys Ile Asn Thr
            195   200   205

His Val Val Tyr Asn His Gln Glu Gln Ala Lys Tyr Glu Asn His Thr
        210   215   220

Glu Asn Ala Leu Leu Leu Tyr Met Ala Cys Thr His Ala Ser Asn Pro
225   230   235   240

Val Tyr Ala Thr Leu Lys Ile Arg Ile Tyr Phe Tyr Asp Ala Val Thr
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Asn


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<213>  Artificial

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<223>  TYLCSV Rep 130 sequence


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<222>  (51)..(443)

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<222>  (231)..(231)
<223>  Point mutation from C (Rep-210 wild-type) to T

<220>
<221>  misc_feature
<222>  (233)..(233)
<223>  Point mutation from C (Rep 210 wild-type) to G

<400>  8
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aga tca ggt cgt ttt agt atc aag gct aaa aat tat ttc ctt aca tat   104
Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu Thr Tyr
       5   10   15

ccc aaa tgt gat tta aca aaa gaa aat gca ctt tcc caa ata aca aac   152
Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile Thr Asn
     20   25   30

cta caa aca ccc aca aac aaa tta ttc atc aaa att tgc aga gaa cta   200
Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg Glu Leu
35   40   45   50

cat gaa aat ggg gaa cct cat ctc cat att ttg atc caa ttc gaa gga   248
His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe Glu Gly
              55   60   65

aaa tac aat tgt acc aat caa cga ttc ttc gac ctg gta tcc cca acc   296
Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Thr
          70   75   80

agg tca gca cat ttc cat ccg aac att cag gga gct aaa tcg agc tcc   344
Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser
          85   90   95

gac gtc aag tcc tat atc gac aag gac gga gat gtt ctt gaa tgg ggt   392
Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu Trp Gly
        100   105   110

act ttc cag atc gac gga cga tct gct agg gga gga caa cag aca gcc   440
Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln Thr Ala
115   120   125   130

tga attc

<210>   9
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<213>   Artificial

<220>
<223>   Synthetic Construct

<400>   9

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             20   25   30

Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg
         35   40   45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe
     50   55   60

Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser
65   70   75   80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser
             85   90   95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu
         100   105   110

Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln
     115   120   125

Thr Ala
    130

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<223>   Primer

<220>
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<223>   Primer for PCR C4 mutagenesis

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<210>   11

<211> 30
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<213> Artificial

<220>
<223> Primer

<220>
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<223> Primer for PCR C4 mutagenesis

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<210> 12
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<213> Geminivirus TYLCSV

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cgtcgatcat ggacttacag gcccatgtat cgaaagccgc ggatgtacag aatgtacaga   180

agccctgatg tacctccggg ttgtgaaggt ccctgtaaag tgcagtcgta cgagcagcgt   240

gatgacgtca agcataccgg tgttgtgcgt tgtgttagtg atgtaactag gggttctggt   300

attactcata gagttggtaa acgtttttgt atcaagtcaa tttatatatt aggaaagatt   360

tggatggatg aaaacataaa aaaacaaaat catactaacc aagtgatgtt tttccttgtt   420

cgagaccgaa ggccttatgg aactagtcct atggattttg gtcaagtttt taacatgttt   480

gataatgaac ccagtactgc tacggtgaag aacgacttac gggataggta tcaagtaatg   540

aggaagtttc atgctacggt tgttggaggt ccgtcaggga tgaaggagca gtgtttgctg   600

aagagatttt ttaaaattaa tacccatgta gtttataatc accaagagca ggcgaagtat   660

gaaaatcata ctgagaatgc cttgttattg tatatggctt gtactcatgc ttctaaccca   720

gtgtacgcta cgttgaaaat acgtatttat ttttatgatg ctgtaacaaa ttaa   774